SEQUENCE LISTING

<110> ZENECA LIMITED

<120> GST SEQUENCES FROM SOYBEAN AND THEIR USE IN THE
      PRODUCTION OF HERBICIDE RESISTANT PLANTS

<130> ZENECA CASE PPD50449/WO

<140>
<141>

<150> GB9922346.3
<151> 1999-09-21

<160> 43

<170> PatentIn Ver. 2.0

<210> 1
<211> 499
<212> PRT
<213> Glycine max

<400> 1

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            20                  25                  30

Arg Ile Asp Gln Lys Leu Leu Gln Asn Ile Val Tyr Asp Ala Leu Val
            35                  40                  45

Trp Ser Thr Leu Asn Cys Leu Leu Val Gly Asp Lys Ser Val Gln Arg
    50                  55                  60

Ser Gly Arg Val Pro Gly Val Gly Leu Val His Leu Pro Leu Ser Leu
 65                  70                  75                  80

Leu Pro Gly Pro Phe Pro Glu Ser His Trp Lys Gln Gly Cys Glu Leu
                85                  90                  95

Ala Pro Ile Phe Asn Glu Leu Val Asp Arg Val Ser Leu Asp Gly Lys
                100                 105                 110

Phe Leu Gln Glu Ser Leu Ser Arg Thr Lys Asn Ala Asp Glu Phe Thr
            115                 120                 125

Ser Arg Leu Leu Asp Ile His Ser Lys Met Leu Gln Ile Asn Lys Lys
    130                 135                 140

Glu Asp Ile Arg Met Gly Ile Val Arg Ser Asp Tyr Met Ile Asp Glu
145                 150                 155                 160

Lys Thr Lys Ser Leu Leu Gln Ile Glu Met Asn Thr Ile Ser Thr Ser
                165                 170                 175

Phe Ala Leu Ile Gly Cys Leu Met Thr Gly Leu His Lys Ser Leu Leu
                180                 185                 190

Ser Gln Tyr Gly Lys Phe Leu Gly Leu Asn Ser Asn Arg Val Pro Ala
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              195                200                  205
Asn Asn Ala Val Asp Gln Ser Ala Glu Ala Leu Ala Lys Ala Trp Ser
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Glu Tyr Asn Asn Pro Arg Ala Ala Ile Leu Val Val Val Gln Val Glu
225             230             235             240
Glu Arg Asn Met Tyr Glu Gln His Tyr Ile Ser Ala Leu Leu Arg Glu
            245             250             255
Lys His His Ile Arg Ser Ile Arg Lys Thr Leu Thr Glu Ile Asp Gln
            260             265             270
Glu Gly Lys Ile Leu Pro Asp Gly Thr Leu Ser Val Asp Gly Gln Ala
            275             280             285
Ile Ser Val Val Tyr Phe Arg Ala Gly Tyr Thr Pro Lys Asp Tyr Pro
    290             295             300
Ser Glu Ser Glu Trp Arg Ala Arg Leu Leu Met Glu Gln Ser Ser Ala
305             310             315             320
Ile Lys Cys Pro Thr Ile Ser Tyr His Leu Val Gly Thr Lys Lys Ile
            325             330             335
Gln Gln Glu Leu Ala Lys Pro Gly Val Leu Glu Arg Phe Val Glu Asn
            340             345             350
Lys Asp His Ile Ala Lys Leu Arg Ala Cys Phe Ala Gly Leu Trp Ser
            355             360             365
Leu Glu Asp Ser Asp Ile Val Lys Lys Ala Ile Glu Asn Pro Glu Leu
    370             375             380
Phe Val Met Lys Pro Gln Arg Glu Gly Gly Gly Asn Asn Ile Tyr Gly
385             390             395             400
Asp Glu Leu Arg Glu Thr Leu Leu Lys Leu Gln Glu Ala Gly Ser Gln
            405             410             415
Glu Asp Ala Ala Tyr Ile Leu Met Gln Arg Ile Phe Pro Ala Thr Ser
            420             425             430
Pro Ala Ile Leu Val Arg Asp Gly Asn Trp Asp Thr Gly His Val Ile
            435             440             445
Ser Glu Ala Gly Ile Phe Gly Thr Tyr Leu Arg Asn Lys Asp Lys Ile
    450             455             460
Ile Ile Asn Asn Glu Ser Gly Tyr Met Val Arg Thr Lys Ile Ser Ser
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Ser Tyr Glu Gly Gly Val Leu Pro Gly Phe Gly Val Val Asp Thr Val
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Tyr Leu Thr
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<213> Artificial Sequence

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<210> 3
<211> 8
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence:Protein
      Fragment

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Cys Phe Ala Gly Leu Trp Ser Leu
 1   5

<210> 4
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Protein
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<400> 4

Val Met Lys Pro Gln Arg Glu Gly Gly Gly Asn Asn Ile Tyr Gly
 1   5   10   15

<210> 5
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Protein
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 1   5   10

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<212> DNA
<213> Glycine max

<400> 6

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ctcaaactca tgtctcaacc tttgaccacc aactctgttc ttgttgaaga ggctgctgct 180

gatggtgatt cctccgccgc cgcacctccc ctcttcgatt atcatcgtat cgaccaaaaa 240

ctgctccaaa acatagttta cgatgctctt gtctggagca ccctcaactg cctccttgtt 300

ggtgacaaat ctgttcagag atcaggaaga gttcctggtg tgggcctggt acatctccca 360

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atgctacaga ttaacaaaaa agaggacata cgcatgggaa tagttcgttc agattatatg 600

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catcatatta gaagcatacg caaaacgttg accgaaattg atcaggaagg aaaaattctg 960

ccagatggaa cactttctgt ggatggacaa gcaatttcag ttgtttactt ccgggctggc 1020

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tcttttaatt gttcctatgg gatggtgtct aattattaac tgtactcaac gacctgtttg 1800

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<210> 7
<211> 222
<212> PRT
<213> Glycine max

<400> 7
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Met Ser Ser Ser Gln Glu Glu Val Thr Leu Leu Gly Val Val Gly Ser
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Pro Phe Leu His Arg Val Gln Ile Ala Leu Lys Leu Lys Gly Val Glu
            20   25   30

Tyr Lys Tyr Leu Glu Asp Asp Leu Asn Asn Lys Ser Asp Leu Leu Leu
        35   40   45

Lys Tyr Asn Pro Val Tyr Lys Met Ile Pro Val Leu Val His Asn Glu
    50   55   60

Lys Pro Ile Ser Glu Ser Leu Val Ile Val Glu Tyr Ile Asp Asp Thr
65   70   75   80

Trp Lys Asn Asn Pro Ile Leu Pro Ser Asp Pro Tyr Gln Arg Ala Leu
                85   90   95

Ala Arg Phe Trp Ala Lys Phe Ile Asp Asp Lys Cys Val Val Pro Ala
            100   105   110

Trp Lys Ser Ala Phe Met Thr Asp Glu Lys Glu Lys Glu Lys Ala Lys
            115   120   125

Glu Glu Leu Phe Glu Ala Leu Ser Phe Leu Glu Asn Glu Leu Lys Gly
    130   135   140

Lys Phe Phe Gly Gly Glu Glu Phe Gly Phe Val Asp Ile Ala Ala Val
145   150   155   160

Leu Ile Pro Ile Ile Gln Glu Ile Ala Gly Leu Gln Leu Phe Thr Ser
            165   170   175

Glu Lys Phe Pro Lys Leu Ser Lys Trp Ser Gln Asp Phe His Asn His
            180   185   190

Pro Val Val Asn Glu Val Met Pro Pro Lys Asp Gln Leu Phe Ala Tyr
    195   200   205

Phe Lys Ala Arg Ala Gln Ser Phe Val Ala Lys Arg Lys Asn
    210   215   220

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<210> 8
<211> 235
<212> PRT
<213> Glycine max

<400> 8
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Met Ala Glu Gln Asp Lys Val Ile Leu His Gly Met Trp Ala Ser Pro
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Tyr Ala Lys Arg Val Glu Leu Ala Leu Asn Phe Lys Gly Ile Pro Tyr
            20   25   30

Glu Tyr Val Glu Glu Asp Leu Arg Asn Lys Ser Asp Leu Leu Leu Lys
        35   40   45

Tyr Asn Pro Val His Lys Lys Val Pro Val Leu Val His Asn Gly Lys
        50   55   60

Ala Ile Ala Glu Ser Met Val Ile Leu Glu Tyr Ile Asp Glu Thr Trp
65   70   75   80

Lys Asp Gly Pro Lys Leu Leu Pro Ser Asp Ser Tyr Lys Arg Ala Gln
                85   90   95

Ala Arg Phe Trp Cys His Phe Ile Gln Asp Gln Leu Met Glu Ser Thr
            100   105   110

Phe Leu Val Val Lys Thr Asp Gly Glu Ala Gln Gln Lys Ala Ile Asp
        115   120   125

His Val Tyr Glu Lys Leu Lys Val Leu Glu Asp Gly Met Lys Thr Tyr
    130   135   140

Leu Gly Glu Gly Asn Ala Ile Ile Ser Gly Val Glu Asn Asn Phe Gly
145   150   155   160

Ile Leu Asp Ile Val Phe Cys Ala Leu Tyr Gly Ala Tyr Lys Ala His
                165   170   175

Glu Glu Val Ile Gly Leu Lys Phe Ile Val Pro Glu Lys Phe Pro Val
            180   185   190

Leu Phe Ser Trp Leu Met Ala Ile Ala Glu Val Glu Ala Val Lys Ile
            195   200   205

Ala Thr Pro Pro His Glu Lys Thr Val Gly Ile Leu Gln Leu Phe Arg
    210   215   220

Leu Ser Ala Leu Lys Ser Ser Ser Ala Thr Glu
225   230   235

<210> 9
<211> 223
<212> PRT
<213> Glycine max

<400> 9

Met Ala Glu Val Lys Leu His Gly Phe Trp Tyr Ser Pro Tyr Thr Leu
    1   5   10   15

Arg Val Val Trp Thr Leu Lys Leu Lys Asp Ile Pro Tyr Gln Asn Ile
                20   25   30

Glu Glu Asp Arg Tyr Asn Lys Ser Leu Gln Leu Leu Glu Tyr Asn Pro
            35   40   45

Val Tyr Lys Lys Thr Pro Val Leu Val His Asn Gly Lys Pro Leu Cys
        50   55   60

Glu Ser Met Leu Ile Val Glu Tyr Ile Asp Glu Ile Trp Ala His Asn
65   70   75   80

Ser Leu Leu Pro Ala Asp Pro Tyr Glu Arg Ala Leu Ala Arg Phe Trp

| | | | 85 | | | | 90 | | | | | 95 | |

Val Lys Tyr Ala Asp Asp Asp Met Phe Ser Ala Val Ile Ala Phe Phe
 100 105 110

Leu Ser Asn Asn Asp Glu Glu Arg Glu Lys Ser Ile Glu Lys Ile Trp
 115 120 125

Glu His Leu Arg Val Val Glu Asn Gln Cys Phe Gly Asp Gln Lys Lys
 130 135 140

Phe Phe Gly Gly Asp Ile Ile Asn Ile Met Asp Ile Ala Phe Gly Ser
145 150 155 160

Ile Phe Lys Ile Leu Val Val Ala Glu Asp Ile Leu Asp Ala Lys Val
 165 170 175

Leu Glu Asp Glu Lys Phe Pro His Leu His Ser Trp Tyr Asn Asn Phe
 180 185 190

Lys Asp Val Ala Val Ile Lys Glu Asn Leu Pro Asp His Glu Lys Met
 195 200 205

Val Ala Phe Ala Lys Phe Ile Arg Glu Lys Arg Leu Ala Cys Thr
 210 215 220

<210> 10
<211> 232
<212> PRT
<213> Glycine max

<400> 10

Met Ala Glu Arg Asp Leu Arg Leu Leu Gly Ala Trp Phe Ser Pro Phe
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Ala Leu Arg Val Gln Ile Ala Leu Asn Leu Lys Gly Leu Asp Tyr Glu
 20 25 30

Val Val Glu Glu Thr Leu Asn Pro Lys Ser Glu Leu Leu Leu Lys Ser
 35 40 45

Asn Pro Val His Lys Lys Ile Pro Val Phe Phe His Gly Asp Lys Val
 50 55 60

Ile Cys Glu Ser Ala Ile Ile Val Glu Tyr Ile Asp Glu Val Trp Ser
65 70 75 80

Asn Asn Ala Leu Ser Ile Leu Pro Gln Asn Ala Tyr Asp Arg Ala Asn
 85 90 95

Ala Arg Phe Trp Val Ser Tyr Ile Asp Asp Lys Trp Leu Thr Ser Leu
 100 105 110

Lys Ser Val Leu Ala Thr Glu Asp Asp Glu Ala Lys Lys Leu His Phe
 115 120 125

Glu Gln Ala Glu Glu Val Leu Glu Lys Val Glu Glu Val Phe Asn Lys
 130 135 140

Cys Ser Glu Gly Lys Ala Tyr Phe Gly Gly Asp Thr Ile Gly Phe Val
145 150 155 160

Asp Ile Gly Phe Gly Ser Phe Leu Ser Phe Ile Arg Val Ser Glu Asn
            165   170   175

Met Asn Glu Arg Lys Leu Leu Asp Glu Thr Lys Tyr Pro Gly Leu Thr
            180   185   190

Leu Trp Ala Glu Thr Phe Ala Ala Asp Pro Ala Val Lys Gly Leu Leu
            195   200   205

Pro Glu Thr Glu Lys Leu Val Glu Phe Ala Lys Ile Leu Gln Leu Lys
            210   215   220

Trp Ala Ala Ala Ala Ala Ala Lys
225   230

<210> 11
<211> 885
<212> DNA
<213> Glycine max

<400> 11

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atttgaacaa caagagtgat ttgctcctca agtataaccc agtttacaaa atgattccag 180

tgcttgttca caatgagaag cccatttcag agtcccttgt gattgttgag tacattgatg 240

acacatggaa aaacaatccc atcttgcctt ctgatcccta ccaaagagcc ttggctcgtt 300

tctgggctaa gttcattgat gacaagtgtg tggttccagc atggaaatct gctttatga 360

ctgatgagaa agagaaagag aaggctaaag aagagttatt tgaggctctg agttttcttg 420

agaatgagtt gaagggcaag tttttttggtg gagaggagtt tggctttgtg gatattgctg 480

ctgtgttaat acctataatt caagagatag cagggttgca attgttcaca agtgagaaat 540

tcccaaagct ctctaaatgg agccaagact ttcacaacca tccagttgtc aacgaagtta 600

tgcctcctaa ggatcaactt tttgcctatt tcaaggctcg ggctcaaagc ttcgttgcta 660

aaagaaagaa ttaatatagt gagactcaga atttccatcg aggtttcagt attgtatgaa 720

atgaaagcta cttgtctatg tttcgttatt gcggttgtat tttcattttt caatgaatta 780

tgtgatatag gatttctcca tgtcaaaaga tagttcaatt caatcaataa aataaacgaa 840

tgagtcgtgt tagagcaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 885

<210> 12
<211> 899
<212> DNA
<213> Glycine max

<400> 12

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aataagagtg atttgcttct aaagtacaac cctgttcaca agaaggttcc tgtacttgtt 180

cataatggaa aggccattgc tgaatccatg gtgatccttg agtatattga tgaaacatgg 240

aaagatggtc ctaaactgct tccaagtgat tcttacaaac gagcccaagc tcgattctgg 300

tgtcatttca tccaggatca gttaatggag agcactttc tagtagtcaa aactgatgga 360

gaagcacaac aaaaggccat tgaccacgtg tatgagaaac tgaaagtgct agaagatgga 420

atgaagacct atctgggaga aggcaatgct attatctctg gtgttgaaaa caactttgga 480

atccttgaca ttgtgttttg tgctttatat ggtgcctaca aggctcatga agaagttatt 540

ggcctcaagt tcatagtgcc agaaaagttt cctgtgttgt tttcttggtt gatggctatt 600

gctgaggttg aagctgtgaa aattgcaact cctccacatg aaaaaacagt gggaattctt 660

cagttgttca ggctgtctgc actgaaatct tcttctgcca cagaatgata tatacttcaa 720

cactttaata gactgtccat cgtttgcttc ttctgcgagt ctttaatgta tgtatctttc 780

aataacagga tgagtaacac ctgagtatgt aaagcgtgat gatatagaga tatacctcta 840

tatatcaaat actcttctat aaacacttct ttctttcctt aaaaaaaaaa aaaaaaaaa 899

<210> 13
<211> 840
<212> DNA
<213> Glycine max

<400> 13

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cttcaacttc ttgaatacaa cccagtatac aagaaaactc cagtgcttgt ccataatgga 180

aaacccttat gtgagtccat gcttattgtt gaatacattg atgagatttg ggcacataat 240

tcattacttc ctgctgatcc ctacgagaga gctctggcaa ggttttgggt taaatatgct 300

gatgatgaca tgttttctgc agttattgca ttcttcctta gcaataatga tgaagagcga 360

gaaaagagca tagagaagat atgggagcat ctcagggttg ttgagaatca gtgttttggt 420

gatcagaaga aattttttgg gggagacatt attaacatta tggacatagc ttttgggtcc 480

atattcaaaa ttcttgtggt tgcagaagat attcttgacg cgaaggtcct ggaagatgag 540

aaattccctc acttgcattc atggtataat aatttcaagg atgttgcagt tattaaagaa 600

aacctcccag accatgagaa aatggtggct tttgctaagt ttattagaga aaaacgtttg 660

gcatgtacct aagaaagtaa tcttatatga gatcaagtat gaatcacttt gtatctgtct 720

gaatcgtttt gttatgcgtg tttctttagt ttccactcca ttattaggat gtcttgacat 780

atctgtgaaa gcaataaaag tttaatggga tgtactggat taaaaaaaaa aaaaaaaaaa 840

<210> 14
<211> 918
<212> DNA
<213> Glycine max

<400> 14

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gttgttgaag agactttgaa tcccaaaagt gaattgcttc ttaagtccaa ccctgtgcac 240

aagaaaatcc cagttttctt ccatggagat aaagtcatat gtgaatctgc aatcatagtt 300

gagtacatag atgaggtttg gtccaacaat gctctctcca tccttccaca aaatgcatat 360

gatcgagcta atgcccgatt ttgggtttct tacatcgatg acaagtggct tacgtccttg 420

aaaagtgttc tagcgactga agatgatgag gcaaagaagc tacactttga gcaagcggaa 480

gaagtgcttg agaaggtgga agaagtgttc aacaagtgca gtgaagggaa ggcctatttc 540

ggaggagata cgattggatt tgttgacatt ggttttggaa gcttttttgag tttcattaga 600

gtctcagaga atatgaatga aagaaaattg cttgatgaaa cgaagtaccc tggtttgacc 660

ctatgggctg aaacttttgc tgctgatcct gctgtgaagg gccttctgcc agagactgaa 720

aagcttgttg agtttgcaaa gattcttcag ctaaaatggg ctgctgcagc tgctgcaaag 780

taaatggaat caaattaatt gctggatgaa tttcaaaaat tgttgtgcaa gttatttata 840

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tatagtaaaa aaaaaaaa   918

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 15

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<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 16

cgcactgaga gaggatcctc gag   23

<210> 17
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> modified base
<222> n=a or t or g or c
<223> Description of Artificial Sequence:PRIMER

<400> 17

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<210> 18
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 18

gagtcymwkg tsattgttga atacattgat gag   33

<210> 19
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 19

cctctcaaac ccatggctca acc   23

<210> 20
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 20

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<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 21

cctctcaaac ccatggctca acc   23

<210> 22
<211> 27
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:PRIMER

<400> 22

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<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PRIMER

<400> 23

gagatctgca acaaacatag cctc   24

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:PRIMER

<400> 24

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<210> 25
<211> 2763
<212> DNA
<213> Artificial Sequence

<220>
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      nucleic acid sequence P32110

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ctttaaataa aaaacattta aagtaaacta taataaaaat atatataaca tgttttaaat 180

aattaaacat taaaataaaa taataacata tcaaataaaa tcacaaaaaa tatactaatg 240

aaatcaactt aatattattt attatatatt taaatatata ttttttaact tttttatttt 300

aaaaaaataa aattgttaac attataaaat taaaaaacaa atttatgaaa aaaaaggtta 360

acaaattaaa aacaaactac aaatagtaaa ataacgtttt taaaaaaaaa aggaggttac 420

gatctcaaaa tcgtatacct catgaaattt ttaaaaaata agtaagacag ttttacaact 480

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ttatatttac attgaagttg taaataatat ttttacgatt tcagttaaaa aaataagaaa 600

actaaaaagt cgtaataggt gctaacaact gttacaactt aacccgtttt agataatttt 660

ttaaaatata ccccaaatga aaaattgcgg attattttat ccccaattgg taaaaaagca 720

cctgaatact agaaacaagg gtggcaaaga ttcaaagtaa tgaatttata aaaaaaaaaa 780

gaaaatattt atataattac acaaaatctt aaaaaatgtt gttattattt actactaatt 840

tataattcga atcgagtata tttaaggcaa agttctctac gcggtttacg taatctctta 900

catcatttat ttttccacgt ttgtttactc tgaggcatct tcttgatagg ggaaagtttt 960

ttcatatttt ttctagatcc ttctcatgtg caatgtctcc gcattcatac gcagcaatca 1020

aaatggaatt aatacacggt agcactttcc catttttttg ttatcgtccc cactattgac 1080

tatacccatg atatgtatat aggtatatct tttctaattg attacgtatc tgctgaatac 1140

tagctagtcc tgattcctag ctctataaaa ggagaatacc ataggaattc atcacagaca 1200

aacaaacaat ttaccagcta tacttgttcc ttttgaaggt tagaagtgct acaatacaaa 1260

caatggcagc tactcaggaa gatgtgaagc ttttgggtat tgtgggaagc ccatttgtgt 1320

gcagggtcca gattgccctt aagttgaagg gagttgaata caaatttttg gaagaaaatt 1380

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catggaagaa caaccccatc ttaccttctg atccttacca aagagccttg gctcgtttct 1560

ggtccaaatt cattgatgat aaggtaactc aacatttcaa aaatcttctt agttttcatg 1620

atttgtgctg atttgtcagc aaaacatcac gatgaaatct atatatgtga aatctttctg 1680

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gctgtatcga aatctgtttt cacggttgat gagaaagagc gtgagaagaa tgttgaagaa 2040

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gctttattct tccttcataa aatccttcaa tgtgcataat cttattcgta gagagactta 2580

gagcggctag tagctactac cttgaaattt tttctttaat tcgaaggaca acgtatatat 2640

tatataataa taattattgc aagttggaaa tcgtgtaagc atgtttcatg actatatgag 2700

ttaacaatat actgtcttgc ctctgcaacc ttcatggatt ctaaaattat tcccttggct 2760

gca   2763

<210> 26
<211> 1137
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mungbean
      Sequence U20809

<400> 26

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gttgaagaaa atttccgcaa caagagtgaa cagcttctga aatacaaccc agttcacaag 180

aaggttccag tgtttgttca tggtgacaaa ccccttccag agtcccttgt gattgttgag 240

tacatcgatg agacatggaa caacaacccc atcttggctt ctgatcctta ccagagagcc 300

ttggctcgtt tctggtccaa attcatcgat gacaagattg tgggtgcttc gtggaaatct 360

gttttcacag ttgatgagaa agagcgtgag aagaatattg cagaaacata tgagagtctg 420

cagtttcttg agaatgagat aaaggagaag aagttctttg gaggagaaga gcttgggttg 480

gtagatattg ctgctgtcta tgtagcattt tggatccctt tgattcaaga aatagcagga 540

ttggagttat tgacaagtga gaaatttcct aatctctaca ggtggagcca agaatttttg 600

aaccatccaa ttgtcaaaga aagtcttccc cctagagacc cagtttttgc cttttttcaaa 660

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accaacaaga ttaagtaagg ctgcattatt tgtcttttttg ttaaattaga tattagtatg 960

caccaaaaag tgagtatttc cttacagaag cttttttaaat attaagtagt taattccata 1020

ggtctaccat tatagctcaa gttatataca tattatgggt gccattctct actcaacaat 1080

tatgactata aaatcttgtg gttataatgc cacgaacaag tgaactatct cacttca   1137

<210> 27
<211> 2038
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Tobacco
      sequence Q03663

<400> 27

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ttggaatgag ataatagaaa agtatgatag tacatgagta acatcaagtt ggaaattaag 240

ggaaggaaat tagagaaaga actgaagaat atccaaatat tctttacgtc caaatttgat 300

agttatttaa cgtcatcgag atgacggcca tgttcaagtt ttccacaaat attgagaaaa 360

gaaagaagaa gacacaaact gtgtttggta ttattatagt tttttctttt agagaattga 420

ttgtacatat aagaaatata atataagatt tagaaataag attattagaa aaatcaaaca 480

tcaaagtatt tattttaaat tcttttttcca atggacattc ccattctgaa aaaaaagaga 540

tataaatatg gaagtaaaaa ttaatcagat cgttaaatgt agaaaatatt aattaacaca 600

ttaaccataa ccagtctact ttatttaaca aaaagcacat ctgaratarc aaaaaagtgt 660

ttaacttcat gcattgacaa tttaaaatta ttttgcaaca tcgggtaaaa ctattttaca 720

acaattggta actgcatata taagtttaat atggtaacct agaaaatagg ataaattatc 780

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gaaacgacct acgtccattt cacgttaata tgtatggatt gttctgcttg atatcaagaa 1500

cttaaataat tgctctaaaa agcaacttaa agtcaagtat atagtaatag tactatattt 1560
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Page 15

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gtaatcctct gaagtggatc tataaaaaga ccaagtggtc ataattaagg ggaaaaatat 1620

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gaatcatgtg ttgatggtct agctacttgc gatattacga gcaaaattct taactacatg 1740

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accaatttag atggtaggag gatattgaaa gtggagcagc tagttttaat aactgaccgt 1860

tagtcttaaa attgacggta taaaaatatt tacataatca ggtcatttat aaggtaatta 1920

taggtaaata tttatgacga attctcaata gtaatctgaa aaaaaattgt aactaaccta 1980

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<210> 28
<211> 2796
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Potato- Derived
      nucleic acid sequence P32111

<400> 28

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aacccaactc aatattagaa aatcaaaaat tttagtgcat tcatttataa aaaaaaaaaa 180

aattacttat gcagttcttg aaccctttgt gagacgagag ggagttgctc ggatggtaag 240

cacccttcac tttcaacccg aaggttgcga gtttgagtca ccaacggagc aaaaagggta 300

ggagctccta gaaagggtaa aaaaaaaaa aaaaattaat aaaaaaatac cctttatgaa 360

atttctcatt ccgctactgc acttctcccc tgatcttcct cgtgttttca attattaatt 420

ctatattcat gacaccatgt gatgtttctc tgggtagtcc taaaaataga ggtattgaaa 480

attatgttgt ttctctctgg tctatttact tttcttgtgt actttattgt atttcatatt 540

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atgttttaat taggtataat acataaatat ttcctttaat tttatctcat tttatattta 720

tgtcgtttaa ctttggagcg tacaagtgtc tacttgtgat ccagtaggtt atcaaagctg 780

gcatgcttag ttttactttc caaattgaaa tttatattag aattgaattc aggaagaatt 840

ttgtaggttc aactaaatta tatatatata tataaaaaaa taaaaattat tagacgcttc 900

gactatttac ttactttaaa atttgaattt tcgtacgaat aaaattattt gtcagagaaa 960

agtcttttag ctattcacat gctaggaagt ttcacttttg gtggatcagt gattgtatat 1020

tatttaatat atatcaattt tctcatcaaa ctgaaaatga aagataaaat taatattaaa 1080
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aaaaataaaa aaagaatatt tctttaacaa attaaaaatg aaaatatgat aaataaatta 1320

aactattcta tcattgattt ttctagccac cagatttgac caaacagtgg gtgacatgag 1380

cacataagtc atctttattg tattttatta ctcactccaa aaatataggg aatatgttta 1440

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aaaattcgac taagacgaac ttctcgtata gtcaacaata ctaacatatt tgtctagtag 2040

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acctcaagtg aatttcaaga ttttgtgtgg caataaaaat tgagtttttg taaattcaat 2700

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<210> 29
<211> 1289
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Arabidopsis
      P46421

<400> 29

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caaagttcgt cgtcgtttta tcacaagacc atcaacacca taaggctata aatccaagct 240

aaaaggtagt gattaactcc acaaaaccag aaaaactaca tttctaacat atagaagaaa 300

cagagaaaaa gagagagaga cccctaatgg ctgagaaaga agaagtgaag cttttgggga 360

tatgggcgag cccttttagc cgtcgggtcg agatggctct caaactcaaa ggcataccgt 420

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aaaattgcat gtcaaataat aaacaattgg ttctgctttg ttaatttatc aaacaagtaa 720

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atatcaatgg caagagcaga cgagaaagga agagaagttt tagccgagca ggtaagagaa 840

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ggattcttgg actttgtcgc cggaagttta attccgtttt gtttggagag aggttgggaa 960

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aatttggaga aggttgagat tgttaaagat tgtgttccac caagagagga acatgtagaa 1080

cacatgaact atatggcaga gagagtgaga tcttcttaag aaaacaaatc atgtttagtt 1140

cttgatcatg caatgtttgt atggttatgt tgttgtttat tttattgaat atctttgtat 1200

gttgtgtggt tgagaagtga ggttttatca tcatctctca cgttatctta tttggtccca 1260

gccactattt agaattaatg gtaaagctt   1289

<210> 30
<211> 1339
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Arabidopsis
      Genomic sequence

<400> 30

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acacatgctc cagggataag gcaaggttag gaattaggac acatctccac ttactaaaaa 120

agagataaaa aaaaattgta tagggaacgt tataaatatg ttgtaaagtc aacatctgtt 180

tccttctaga ctcttcgcat ttacatcaca ctgccgacca tataaaacgg caaagttcgt 240

cgtcgtttta tcacaagacc atcaacacca taaggctata aatccaagct aaaaggtagt 300

gattaactcc acaaaaccag aaaaactaca tttctaacat atagaagaaa cagagaaaaa 360

gagagagaga cccctaatgg ctgagaaaga agaagtgaag cttttgggga tatgggcgag 420

cccttttagc cgtcgggtcg agatggctct caaactcaaa ggcataccgt acgagtacgt 480

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agtccctgtt cttgtccaca atggtaaaac cattctcgag tctcatgtga ttcttgaata 600

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actttgtcgc cggaagttta attccgtttt gtttggagag aggttgggaa ggaataggat 1020

tggaagtgat tacagaggag aagtttccag agttcaagag atgggttagg aatttggaga 1080

aggttgagat tgttaaagat tgtgttccac caagagagga acatgtagaa cacatgaact 1140

atatggcaga gagagtgaga tcttcttaag aaaacaaatc atgtttagtt cttgatcatg 1200

caatgtttgt atggttatgt tgttgtttat tttattgaat atctttgtat gttgtgtggt 1260

tgagaagtga ggtttttatca tcatctctca cgttatctta tttggtccca gccactattt 1320

agaattaatg gtaaagctt   1339

<210> 31
<211> 968
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Papaya AJ000923

<400> 31

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gctccgtttt acaacaatgg cggacgaggt tgttctcttg gatttctggc caagcccttt 120

tggaatgaga atcagaatcg ctttagccga gaagggtatt cactacgagt acaaggaaga 180

gaatctgaga aacaagagtc ccttactcct gcagatgaac ccggtacaca agaaaatccc 240

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agaggcagaa tgccccaagt tgtttagttg ggtgaaaagg tgtttggaga aggagagtgt 660

ttcaaaatct ctgcctgatc aagataaggt atacggcttc gttttggaac tcaggaaggc 720

tcttgggatt tgagtttttt gagagacttc aaaatccttg ttccatttcc attagggttc 780

gtcctccaag tattgattaa aaaaggttct ggatcaacta ctttatttgt ctagtctttt 840

actgttgtat tggaataaag gggtgtcctt ttgtggatta ggtgagattt ctatcaatat 900

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<210> 32
<211> 1040
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Spruce AF051214

<400> 32

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tgctgcgggt ccgtatagca cttgctctta aagggatcga ttacgagttc atcgaagaga 180

acatgcaaaa taagagccat ctgctgctgc aatcgaaccc tgttaacaag aagattccag 240

tgctcatcca caatggaaag cctgtttgtg agtccatgat tattgtgcag tacatagacg 300

aggcatggga cacgaaggcg ccagttctaa tgcccaaaga tccttatgac cgagccattg 360

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atcgattctg tgaggccgat ggagtgaaag acgttatgcc ggatccggcc aagttgcagg 720

aatttatatc cgccatcaga gtcagattta catcaccacc tgctgccaat taggggaagc 780
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cattcggcca ttaaatggat gttatcgtcc gcattgtttt tggttttatg ctgtcagttt 840

gaatgttgtt atgctttttg aattgttggt gtttaatggg aataattcta tcgcccaatc 900

tagcaccgtg tgattcgcta tcagttctca ccgtgttcca tgtaacttcg atttcatgat 960

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<210> 33
<211> 902
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Wheat AF004358

<400> 33

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acactgacac acatcgatcg aggtagttag agatggccgg aggagatgac ctgaagctgc 120

tcggcgcatg gccaagccca tttgttacca gggtgaagct ggcgctcgcc ctgaagggcc 180

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tagccccatg gaggcagtgg ttgaggggca agacagagga ggagaaatcc gagggaaaga 480

agcaggcgtt cgccgcggtg ggggtcctcg aaggggccct gagggagtgc tccaagggag 540

ggggcttctt cggtggcgac ggcgtcgggc tcgtcgacgt tgcgctggga ggcgtgctgt 600

cgtggatgaa ggtgaccgag gcgctgtctg gtgacaagat tttcgacgcc gccaagactc 660

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aa   902

<210> 34
<211> 1127
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Spruce AF051238

<400> 34

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cgtgctgcgg gttcgcatag cacttgctct taaaggcatc gattacgagt tcatcgaaga 180

gaacatgcaa aataggagcc agctgctgct gcaatcaaac cctgttcaca ggaagattcc 240

agtgcttatc cacaatggaa agcccgtttg tgaatccatg attattgtgc agtacatcga 300

tgaggcatgg gacactaagg cacccaatct tatgcccaaa gatccatatg acctagccat 360

tgcccgcttc tgggctgcct ttgtagacga taagctcgtt ccatgtatgc ggagagtttt 420

cgctggccat ggcgagcagc tacagaaaga agcggaagat ctggttacaa actttcattt 480

gatagaggaa gctctgcgaa ccaacagctg cttctcagga aaagcgtatt ttggagggga 540

taagataggc ttgcttgaca tcgcattggg tggtatgttg gcggttctca aaggcctcga 600

gaaggctacc gataccgtta aatagatcc ggagaagatg ccgttgctga gcgcatggat 660

ggaccgattt tgtcaatcca atggagtgaa agaagtaatg cccgatccgg ccaagcagct 720

ggaatctcta tcagctagga gagccagact tgcatcacct gctggcaatt agggcaagcc 780

atgtcggcct tataaactga ggatagacag atggattata aacttattat tcgtagtact 840

tgtcctttta ttcatgtggt cagcttcagc gttttaattc ttgctgtttt atgtgaataa 900

gtctgaataa tgtttgggtg aatctcgcct gtactatagc tggcattcac ctgtttattg 960

tacgctgatt tagtttgaac aagtttggt gaatctcccc tgtactgaag ctggcattcc 1020

cctgttcaat gtgcgctgat ttagtttgaa taagtttttg atgaatctcg cttgtactgt 1080

agctatgtgc gatgattttt aatgccatag aaacgagaat gaaatgc 1127

<210> 35
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 35

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<210> 36
<211> 234
<212> PRT
<213> Glycine max

<400> 36

Met Ser Lys Ser Glu Asp Leu Lys Leu Leu Gly Gly Trp Phe Ser Pro
 1   5   10   15

Phe Ala Leu Arg Val Gln Ile Ala Leu Asn Leu Lys Gly Leu Glu Tyr
            20   25   30

Glu Val Val Glu Glu Thr Leu Asn Pro Lys Ser Asp Leu Leu Leu Lys

```
            35                    40                      45
Ser Asn Pro Val His Lys Lys Ile Pro Val Phe Phe His Gly Asp Lys
        50              55              60
Val Ile Cys Glu Ser Ala Ile Ile Val Glu Tyr Ile Asp Glu Ala Trp
65              70              75                      80
Thr Asn Val Pro Ser Ile Leu Pro Gln Asn Ala Tyr Asp Arg Ala Asn
                85              90                      95
Ala Arg Phe Trp Phe Ala Tyr Ile Asp Glu Lys Trp Phe Thr Ser Leu
            100             105             110
Arg Ser Val Leu Val Ala Glu Asp Asp Glu Ala Lys Lys Pro His Phe
        115             120             125
Glu Gln Ala Glu Glu Gly Leu Glu Arg Leu Glu Glu Val Phe Asn Lys
    130             135             140
Tyr Ser Glu Gly Lys Ala Tyr Phe Gly Gly Asp Ser Ile Gly Phe Ile
145             150             155             160
Asp Ile Gly Phe Gly Ser Phe Leu Ser Trp Met Arg Val Ile Glu Glu
            165             170             175
Met Ser Gly Arg Lys Leu Leu Asp Glu Lys Lys His Pro Gly Leu Thr
            180             185             190
Gln Trp Ala Glu Thr Phe Ala Ala Asp Pro Ala Val Lys Gly Ile Leu
        195             200             205
Pro Glu Thr Asp Lys Leu Val Glu Phe Ala Lys Ile Leu Gln Leu Lys
    210             215             220
Trp Thr Ala Ala Ala Ala Ala Ala Lys
225             230
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<210> 37
<211> 222
<212> PRT
<213> Glycine max

<400> 37

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  1           5               10                      15
Pro Phe Leu His Arg Val Gln Ile Ala Leu Lys Leu Lys Gly Val Glu
            20              25              30
Tyr Lys Tyr Leu Glu Asp Asp Leu Asn Asn Lys Ser Asp Leu Leu Leu
        35              40              45
Lys Tyr Asn Pro Val Tyr Lys Met Ile Pro Val Leu Val His Asn Glu
        50              55              60
Lys Pro Ile Ser Glu Ser Leu Val Ile Val Glu Tyr Ile Asp Asp Thr
65              70              75                      80
Trp Lys Asn Asn Pro Ile Leu Pro Ser Asp Pro Tyr Gln Arg Ala Leu
                85              90                      95
```

Ala Arg Phe Trp Ala Lys Phe Ile Asp Asp Lys Cys Val Val Pro Ala
          100   105   110

Trp Lys Ser Ala Phe Met Thr Asp Glu Lys Glu Lys Glu Lys Ala Lys
          115   120   125

Glu Glu Leu Phe Glu Ala Leu Ser Phe Leu Glu Asn Glu Leu Lys Gly
   130   135   140

Lys Phe Phe Gly Gly Glu Glu Phe Gly Phe Val Asp Ile Ala Ala Val
145   150   155   160

Leu Ile Pro Ile Ile Gln Glu Ile Ala Gly Leu Gln Leu Phe Thr Ser
          165   170   175

Glu Lys Phe Pro Lys Leu Ser Lys Trp Ser Gln Asp Phe His Asn His
          180   185   190

Pro Val Val Asn Glu Val Met Pro Pro Lys Asp Gln Leu Phe Ala Tyr
          195   200   205

Phe Lys Ala Arg Ala Gln Ser Phe Val Ala Lys Arg Lys Asn
   210   215   220

<210> 38
<211> 895
<212> DNA
<213> Glycine max

<400> 38

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gtctagaata tgaggttgtt gaagagacct tgaatcccaa aagtgacctg cttcttaagt 180

ccaaccctgt gcacaagaaa atcccagttt tcttccatgg agataaagtc atttgtgaat 240

ctgcaatcat agttgagtac attgatgagg cttggactaa tgttccctcc atccttccac 300

aaaatgctta tgatcgtgct aatgctcgat tttggtttgc ctacattgat gagaagtggt 360

ttacgtcctt gagaagtgtt ctagtggctg aagatgatga ggcaaagaag ccacactttg 420

agcaagcaga agaagggctt gagaggttgg aagaagtgtt caacaagtac agtgaaggga 480

aggcctattt cggaggagat agcattggat tcattgacat tggttttggg agcttcttga 540

gttggatgag agtcatagag gagatgagtg gaagaaaatt gcttgatgaa aagaagcacc 600

ctggtttgac ccaatgggct gaaacgtttg ctgctgatcc tgctgtgaag ggcattcttc 660

cagagactga taagcttgtt gagtttgcca gattcttca gctaaaatgg actgctgcag 720

cagctgcagc tgcaaagtaa atggaatcaa attaattgcg agagtatttt caaaattgtt 780

gtccaagttg tttttatctc aggctatgtt gttgcaactt tatttattta aaagttattt 840

taaatttaaa atgtaaaata ttaagaaagt ttaagtaagt tagttgaaaa atttt 895

<210> 39
<211> 895
<212> DNA
<213> Glycine max

<400> 39

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agattgctct caagttgaag ggagttgaat acaaatattt ggaagacgat ttgaacaaca 180

agagtgattt gctcctcaag tataacccag tttacaaaat gattccagtg cttgttcaca 240

atgagaagcc catttcagag tcccttgtga ttgttgagta cattgatgac acatggaaaa 300

acaatcccat cttgccttct gatccctacc aaagagcctt ggctcgtttc tgggctaagt 360

tcattgatga caagtgtgtg gttccagcat ggaaatctgc ttttatgact gatgagaaag 420

agaaagagaa ggctaaagaa gagttatttg aggctctgag ttttcttgag aatgagttga 480

agggcaagtt ttttggtgga gaggagtttg gctttgtgga tattgctgct gtgttaatac 540

ctataattca agagatagca gggttgcaat gttcacaag tgagaaattc ccaaagctct 600

ctaaatggag ccaagacttt cacaaccatc cagttgtcaa cgaagttatg cctcctaagg 660

atcaactttt tgcctatttc aaggctcggg ctcaaagctt cgttgctaaa agaaagaatt 720

aatatagtga gactcagaat ttccatcgag gtttcagtat tgtatgaaat gaaagctact 780

tgtctatgtt tcgttattgc ggttgtattt tcatttttca atgaattatg tgatatagga 840

tttctccatg tcaaaagata gttcaattca atcaataaaa taaacgaatg agcgg   895

<210> 40
<211> 977
<212> DNA
<213> Glycine max

<400> 40

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gaagctttttg ggagctactg gaagcccatt tgtgtgcagg gttcagattg ccctcaagtt 180

gaagggagtt caatacaaat ttttggaaga aaatttgagg aacaagagtg aactgcttct 240

caaatccaac ccagttcaca agaaggttcc agtgtttatt cacaatgaga gcccatagc 300

agagtctctt gtgattgttg aatacattga tgagacatgg aagaacaacc ccatcttgcc 360

ttctgatcct taccaaagag ccttggctcg tttctggtcc aaattcattg atgacaaggt 420

tgtgggtgct gcatggaaat atatttatac tgttgatgag aaagagcgtg agaagaatgt 480

tgaagagtca tatgaggctc tgcagtttct tgagaatgag ctgaaggaca gaagttttt 540

tggaggagag gaaattgggt tggtagatat tgctgctgtc ttcatagcat tttggatccc 600

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tataattcaa gaagtattgg gtttgaagtt attcacaagt gagaaatttc ctaagctcta  660

caaatggagc caagagttca tcaaccaccc tgttgtcaaa caagtccttc ctcctagaga  720

tcaacttttt gccttctaca aagcctgcca tgaaagtctt tctgcttcaa aatagactta  780

tttaaggata gttgtgtgaa ctactggtct ctcatttgtg agttattgca gtttgaattt  840

catgtcaatt tggttttata tgtaatttag taacctggga tatctcccat ggagaaaata  900

atccttggat cttgtttcca ttttggccat ttcagttaat aaagaaattc attttttcca  960

aaaaaaaaaa aaaaaaa                                                   977
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<210> 41
<211> 1006
<212> DNA
<213> Glycine max

<400> 41
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aagaaaattt gaggaacaag agtgaactgc ttctcaaatc caacccagtt cacaagaagg  180

ttccagtgtt tattcacaat gagaagccca tagcagagtc tcttgtgatt gttgaataca  240

ttgatgagac atggaagaac aaccccatct tgccttctga tccttaccaa agagccttgg  300

ctcgtttctg gtccaaattc attgatgata aggtttttgg tgctgcatgg aaatccgttt  360

tcacagctga tgagaaagag cgtgagaaga atgttgagga agcaattgag ctctgcagtt  420

tcttgagaat gagataaagg acaagaagtt ctttggagga gaggagattg ggttggtaga  480

tattgctgct gtctacatag cattttgggt ccctatggtt caagaaattg cagggttgga  540

gttattcaca agtgagaaat ttcctaagct ccacaattgg agccaagaat ttttgaacca  600

tccaattgtc aaagaaagtc tgccccctag agatcctgtt ttctcctttt tcaagggtct  660

ctatgaaagc cttttttggtt caaaatagat ttgatgatgt ggtgtgagac ttagtatttc  720

taagaattat gtgtttgtta aaggcttcta tgaaagcctc actgcttcaa aatagattca  780

tgtatgtgag actcagaatc tctggggaaa attgtgtgtg gtgtggacta cttgttttgt  840

ttgtcattga gctatatcgc tgttaattag gattttgttt caaaatgatg cttataagtt  900

gtaatctagg atttctccct ttgaaatcct aggttgttct tgacatttgc tatttcaaag  960

aataaatata tagcatcttt ctatttctca aaaaaaaaaa aaaaaa            1006
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<210> 42
<211> 885
<212> DNA
<213> Glycine max

<400> 42
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ccaagagggt ggaattggcc cttaatttta agggcatacc ctatgagtat gttgaagaag 120

acttgagaaa taagagtgat ttgcttctaa agtacaaccc tgttcacaag aaggttcctg 180

tacttgttca taatggaaag gccattgctg aatccatggt gatccttgag tatattgatg 240

aaacatggaa agatggtcct aaactgcttc caagtgattc ttacaaacga gcccaagctc 300

gattctggtg tcatttcatc caggatcagt taatggagag cacttttcta gtagtcaaaa 360

ctgatggaga agcacaacaa aaggccattg accacgtgta tgagaaactg aaagtgctag 420

aagatggaat gaagacctat ctgggagaag gcaatgctat tatctctggt gttgaaaaca 480

actttggaat ccttgacatt gtgttttgtg ctttatatgg tgcctacaag gctcatgaag 540

aagttattgg cctcaagttc atagtgccag aaaagtttcc tgtgttgttt tcttggttga 600

tggctattgc tgaggttgaa gctgtgaaaa ttgcaactcc tccacatgaa aaaacagtgg 660

gaattcttca gttgttcagg ctgtctgcac tgaaatcttc ttctgccaca gaatgatata 720

tacttcaaca ctttaataga ctgtccatcg tttgcttctt ctgcgagtct ttagtgtatg 780

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<210> 43
<211> 991
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SSM.PK0067.G5

<400> 43

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aagaagaagt gaggctattg ggcaagtggg ccagcccatt tagcaacaga gtagaccttg 180

ctctcaagct caagggtgtt ccctacaaat actccgagga agatcttgct aacaagagtg 240

ctgatcttct caagtacaac cccgttcaca agaaggttcc ggttttggtc cacaatggga 300

acccattgcc cgagtcactc atcattgttg aatacataga tgagacgtgg aaaaataacc 360

cactattgcc tcaagaccca tatgaaagag ccttggctcg tttttggtct aagaccttag 420

atgacaagat cttgccagct atatggaatg cttgctggag tgacgagaat gggcgtgaga 480

aagcagtgga ggaagccttg gaagcattga aaatcctaca ggaaacactg aaagacaaga 540

aattctttgg aggagagagc ataggattgg tagatattgc tgccaatttc attgggtatt 600

gggttgccat attgcaagag attgcagggt tggagttgct caccattgag aaatttccca 660

agttatataa ttggagtcaa gactttatca accaccctgt gatcaaggag ggtctgcctc 720
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ctagagatga attgtttgct ttcttcaaag cttctgctaa aaagtagaac cattttagag 780
gtaggattca taataagtta gtatgatttt gttgggaaac aattatcttg ttgtgagcaa 840
aggattgttc tgttttaaat ttaattgact gtgatttggt tgggtattgg ctattttaat 900
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a                             991
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